

GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2006, 22:56:42 ; Search time 2483 Seconds

(without alignments)  
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Title: US-10-824-036A-3578

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	35	14	100.0	23	2	CS102434	Sequence
	36	14	100.0	23	2	CS137028	Sequence
	37	14	100.0	24	2	CS094008	Sequence
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ACCESSION CQ967218  
VERSION CQ967218.1 GI:5614984  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Mcswiggen, J., Beigelman, L., Uman, N., Haerberli, P., Chowrira, B. and Polisky, B.  
TITLE RNA interference mediated inhibition of MAP kinase gene expression using short interfering nucleic acid (siNA)  
JOURNAL Patent: WO 2004097(20-A 1858 11-NOV-2004;  
Sirma Therapeutics, Inc (US)  
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DEFINITION Sequence 218 from Patent WO2004111237.  
ACCESSION CQ974653  
VERSION CQ974653.1 (..57998833

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KEYWORDS
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ORGANISM    synthetic construct
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REFERENCE   1
AUTHORS     McSwiggen,J. and Chowrira,B.
TITLE       RNA interference mediated inhibition of platelet-derived
            endothelial cell growth factor (ECGF1) gene expression using short
            interfering nucleic acid (siNA)
JOURNAL     Patent: WO 200411237-A 258 23-DEC-2004;
            Sirna Therapeutics, Inc. (US)
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Sequence 1901 from Patent WO2005003350.
ACCESSION CQ989002
VERSION   CQ989002.1 GI:58196690
KEYWORDS
SOURCE   synthetic construct
ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE 1
AUTHORS   McSwiggen,J. and Beigelman,L.
TITLE     RNA interference mediated treatment of Alzheimer's disease using
            short interfering Nucleic Acid (siNA)
JOURNAL   Patent: WO 2005003350-A 1901 13-JAN-2005;
            Sirna Therapeutics, Inc. (US)
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DEFINITION
Sequence 295 from Patent WO2005007855.
ACCESSION CS010063
VERSION   CS010063.1 GI:59669892
KEYWORDS
SOURCE   synthetic construct
ORGANISM synthetic construct
            other sequences; artificial sequences.

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REFERENCE   1
AUTHORS     Uman,N. and Mcswiggen,J.
TITLE       RNA interference mediated inhibition of B7-H1 gene expression using
            short interfering Nucleic Acid (siNA)
JOURNAL     Patent: WO 2005007855-A 295 27-JAN-2005;
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Sequence 952 from Patent WO2005007859.
ACCESSION CS15515
VERSION   CS15515.1 GI:59675319
KEYWORDS
SOURCE   synthetic construct
ORGANISM synthetic construct
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REFERENCE 1
AUTHORS     Mcswiggen,J. and Uman,N.
TITLE       RNA interference mediated inhibition of acetyl-coa-carboxylase gene
            expression using short interfering nucleic acid (siNA)
JOURNAL     Patent: WO 2005007859-A 952 27-JAN-2005;
            Sirna Therapeutics, Inc. (US)
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ACCESSION CS028804
VERSION   CS028804.1 GI:60498345
KEYWORDS
SOURCE   synthetic construct
ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE 1
AUTHORS     Mcswiggen,J. and Chowrira,B.M.
TITLE       RNA interference mediated inhibition of XIAP gene expression using
            short interfering Nucleic Acid (siNA)
JOURNAL     Patent: WO 2005014811-A 1057 17-FEB-2005;

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CS091306          14 bp RNA linear PAT 25-MAY-2005
LOCUS
DEFINITION
Sequence 2028 from Patent WO2005028650.
ACCESSION
CS091306
VERSION
CS091306.1 GI:66716563
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
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AUTHORS
Jadhav,V., Kossen,K., Zinnen,S., Vaish,N. and Mcswiggen,J.
TITLE
RNA interference mediated inhibition of Hepatitis C Virus (HCV)
expression using short interfering Nucleic Acid (siNA)
JOURNAL
Patent: WO 2005028650-A 2028 31-MAR-2005;
SiRNA Therapeutics, Inc. (US)
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Db 1 ATATATCTATTTCG 14

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CS091762          14 bp RNA linear PAT 03-JUN-2005
LOCUS
DEFINITION
Sequence 371 from Patent WO2005045034.
ACCESSION
CS091762
VERSION
CS091762.1 GI:66949338
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
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AUTHORS
Mcswiggen,J., Haeblerli,P. and Beigelman,L.
TITLE
RNA interference mediated treatment of Parkinson disease using
short interfering Nucleic Acid (siNA)
JOURNAL
Patent: WO 2005045034-A 371 19-MAY-2005;
SiRNA Therapeutics, Inc. (US)
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LOCUS
DEFINITION
Sequence 471 from Patent WO2005045032.
ACCESSION
CS092397
VERSION
CS092397.1 GI:66949935
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct; artificial sequences.
REFERENCE
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AUTHORS
Usman,N. and McSWIGGEN,J.
TITLE
RNA interference mediated inhibition of early growth response gene
expression using short interfering Nucleic Acid (siNA)
JOURNAL
Patent: WO 2005045032-A 471 19-MAY-2005;
SiRNA Therapeutics, Inc. (US)
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DEFINITION
Sequence 455 from Patent WO2005045039.
ACCESSION
CS092855
VERSION
CS092855.1 GI:66950384
KEYWORDS
synthetic construct
SOURCE
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ORGANISM
synthetic construct; artificial sequences.
REFERENCE
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AUTHORS
Richards,I., and McSWIGGEN,J.
TITLE
RNA interference mediated inhibition of intercellular adhesion
molecule (ICA) gene expression using short interfering Nucleic
Acid (siNA)
JOURNAL
Patent: WO 2005045039-A 455 19-MAY-2005;
SiRNA Therapeutics, Inc. (US)
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 VERSION CS094005.1 GI:66951519  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 McSwiggen, J. RNA interference mediated inhibition of hairless (hr) gene expression using short interfering nucleic acid (siRNA)  
 TITLE Patent: WO 2005045036-A 1139 19-MAY-2005;  
 JOURNAL Sirna Therapeutics, Inc. (US)  
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 ACCESSION CS094006  
 VERSION CS094006.1 GI:66951520  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 McSwiggen, J. RNA interference mediated inhibition of hairless (hr) gene expression using short interfering nucleic acid (siRNA)  
 TITLE Patent: WO 2005045036-A 1140 19-MAY-2005;  
 JOURNAL Sirna Therapeutics, Inc. (US)  
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 ACCESSION CS094331  
 VERSION CS094331.1 GI:66951836  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 McSwiggen, J. and Polisky, B. RNA interference; mediated inhibition of cholesterol ester transfer protein (cetp) gene expression using short interfering nucleic acid (siRNA)  
 TITLE Patent: WO 2005045041-A 323 19-MAY-2005;  
 JOURNAL Sirna Therapeutics, Inc. (US)  
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 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 McSwiggen, J., Chowrira, B.M. and Haerberli, P. RNA interference mediated inhibition of NOGO and NOGO receptor gene expression using short interfering Nucleic Acid (siNA)  
 TITLE Patent: WO 2005045035-A 321 19-MAY-2005;  
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ACCESSION CS095630
VERSION CS095630.1 GI:66952208
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS McSwiggen,J., Chowira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene
expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 322 19-MAY-2005;
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Job time : 2483 secs

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GenCore version 5.1.9  
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Run on: June 28, 2006, 22:55:31 ; Search time 302 Seconds  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	31	14	100.0	14	AEA12246	Aea12246 Exemplary
	32	14	100.0	14	AEBO6727	Aeb06727 Target se
	33	14	100.0	14	AEA42929	Aea42929 Exemplary
c	34	14	100.0	14	AEA42930	Aea42930 Exemplary
	35	14	100.0	14	AEA39911	Aea39911 Target se
	36	14	100.0	14	AEBO9186	Aeb09186 Human alp
	37	14	100.0	14	AEBO17833	Aeb17833 G72 RNA i
c	38	14	100.0	14	AEBO17834	Aeb17834 G72 RNA i
	39	14	100.0	14	AEBO6056	Aeb06056 Target se
	40	14	100.0	14	AEBO72668	Aeb72668 Exemplary
	41	14	100.0	14	AEBO16265	Aeb16265 Human tel
	42	14	100.0	14	AEBO25202	Aeb25202 Human MDR
	43	14	100.0	14	AEBO43829	Aeb43829 Novel hum
c	44	14	100.0	14	AEBO26386	Aeb26386 Target-co
	45	14	100.0	14	AEBO26385	Aeb26385 Target se

ALIGNMENTS

RESULT 1  
ADT66481  
ID ADT66481 standard; RNA; 14 BP.  
XX  
AC ADT66481;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Target sequence containing 5' palindrome/repeat.  
XX  
KW siRNA; short interfering RNA; ss; RNA interference; gene silencing.  
XX  
OS Synthetic.  
XX  
FN WO2004092383-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 13-APR-2004; 2004WO-US011320.  
XX  
PR 15-APR-2003; 2003US-0462874P.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 14-JAN-2004; 2004US-00757803.  
XX  
(SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Bharat C, Haeberli P;  
XX  
DR WPI; 2004-766879/75.  
XX  
PT Novel chemically synthesized double stranded short interfering nucleic  
PT acid molecule directing cleavage of severe acute respiratory syndrome  
PT virus RNA through RNA interference, useful for treating viral infection.  
XX  
PS Disclosure; Fig 14; 219pp; English.  
XX  
CC The invention relates to a chemically synthesised double stranded short  
interfering ribonucleic acid (siRNA) molecule directing cleavage of

CC severe acute respiratory syndrome (SARS) virus RNA through RNA  
 CC interference, comprising a strand having nucleotide sequence with  
 CC sufficient complementarity to the SARS virus RNA to direct cleavage of  
 CC the SARS virus RNA through RNA interference, where the siRNA does not  
 CC require the presence of nucleotides having a 2'-hydroxy group for  
 CC mediating RNA interference, and each strand of is 19-23 nucleotides in  
 CC length. The siRNA is useful for modulating the expression of genes of  
 CC associated with the development or maintenance of SARS virus infection,  
 CC acute respiratory failure, viral pneumonia and/or disease states  
 CC associated with SARS virus infection, and for treating SARS virus  
 CC infection, acute respiratory failure, viral pneumonia and/or disease  
 CC states associated with SARS virus infection by preventing the  
 CC transcriptions of SARS gene. The siRNA is useful in diagnosis, and  
 CC treatment of diseases and conditions that respond to the modulation of  
 CC SARS virus gene expression and/or activity. The siRNA is useful in  
 CC therapeutic, diagnostic, target validation, genomic discovery, genetic  
 CC engineering, and pharmacogenomic applications. The siRNA is stable and  
 CC capable of mediating RNA interference against SARS inside a cell or  
 CC reconstituted in vitro system, and has high degree of specificity with  
 CC respect to SARS RNA expression. The present sequence is sequence used to  
 CC illustrate the principle of designing siRNA molecules based on  
 CC palindromic or repeat containing target sequences.

SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 13; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
 |||||  
 DB 1 AUAUAUCUAUUUCG 14

## RESULT 2

ID ADU66346  
 ADU66346 standard; RNA; 14 BP.

XX AC ADU66346;

DT 27-JAN-2005 (first entry)

XX Palindrome utilizing duplex oligonucleotide exemplary sequence #1.

XX RNA interference; mitogen activated protein kinase inhibitor;  
 KW inflammation; immunosuppressive; immune disorder; autoimmune disease;  
 KW allergy; antiallergic; cytostatic; neoplasm; cancer; ss.

XX Synthetic.

PN WO2004097020-A2.

XX 11-NOV-2004.

PF 23-APR-2004; 2004WO-US012517.

XX 25-APR-2003; 2003US-00424339.

PR 30-APR-2003; 2003US-00427160.

PR 23-MAY-2003; 2003US-00444853.

PR 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 14-JAN-2004; 2004US-00757803.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Usman N, Haeblerli P, Chowrira B;

PI Polisky B;

XX WPI; 2005-012649/01.

XX Novel short interfering nucleic acid molecule useful for inhibiting  
 PT mitogen activated protein kinase gene expression e.g., c-JUN associated  
 PT with diseases e.g., inflammatory disease or autoimmune disease.

XX Disclosure; SEQ ID NO 1858; 322pp; English.

XX The invention relates to a chemically synthesized double stranded short  
 CC interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a c  
 CC -JUN RNA through RNA interference (RNAi), where one strand of the siRNA  
 CC molecule comprises nucleotide sequence having sufficient complementarity  
 CC to the c-JUN RNA for the siRNA molecule to direct cleavage of the c-JUN  
 CC RNA through RNA interference. (I) is useful for inhibiting mitogen  
 CC activated protein kinase gene (e.g., c-JUN, JNK1, JNK2, p38, ERK1 or  
 CC ERK2) expression associated with diseases e.g., inflammatory disease,  
 CC autoimmune disease, allergy, cancer. (I) exhibits improved RNA  
 CC interference activity and nuclease resistance. The present sequence  
 CC represents a palindrome utilizing duplex oligonucleotide exemplary  
 CC sequence.

SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
 |||||  
 DB 1 AUAUAUCUAUUUCG 14

## RESULT 3

ADV60863

ID ADV60863 standard; RNA; 14 BP.

XX AC ADV60863;

XX 10-MAR-2005 (first entry)

XX Duplex forming oligonucleotide, target sequence.

XX ss; gene silencing; siRNA; short interfering RNA; RNA interference;  
 KW DNA-RNA hybrid.

XX Synthetic.

XX WO2004111237-A1.

XX 23-DEC-2004.

XX 16-APR-2004; 2004WO-US011848.

XX 16-APR-2003; 2003US-00417012.

PR 24-APR-2003; 2003US-00422704.

PR 30-APR-2003; 2003US-00427160.

PR 23-MAY-2003; 2003US-00444853.

PR 29-AUG-2003; 2003US-00652791.

PR 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 14-JAN-2004; 2004US-00757803.

PR 13-FEB-2004; 2004US-00780447.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Chowrira B;

XX WPI; 2005-040107/04.

XX New chemically synthesized double stranded short interfering ribonucleic  
 PT acid (siRNA), useful in preparing a composition for inhibiting platelet-  
 PT derived endothelial cell growth factor (ECFGI) gene expression for  
 PT treating e.g., cancer.

XX Disclosure; Fig 14; 197pp; English.

XX The invention relates to a new chemically synthesized double stranded  
 CC short interfering ribonucleic acid (siRNA) molecule directs cleavage of a



```

CC platelet-derived endothelial cell growth factor (ECGF1) RNA via RNA
CC interference (RNAi). Also included is a composition comprising the siRNA
CC molecule in a carrier or diluent. The siRNA molecule is useful in
CC preparing a composition for inhibiting platelet-derived endothelial cell
CC growth factor (ECGF1) gene expression for treating proliferative diseases
CC e.g., cancers, lymphomas, carcinomas, sarcomas, tumor angiogenesis,
CC macular degeneration, corneal neovascularization, diabetic retinopathy,
CC neovascular glaucoma, myopic degeneration, restenosis and polycystic
CC kidney disease. The present sequence is a sequence used to illustrate
CC duplex forming oligonucleotides which incorporate a palindrome or repeat
CC sequence and their use as siRNAs.
XX
SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14
DB 1 AUAUAUCUAUUUCG 14

RESULT 4
ADW28003
ID ADW28003 standard; RNA; 14 BP.
AC ADW28003;
XX
XX 07-APR-2005 (first entry)
DE Cholinergic receptor muscarinic 3 gene targeted siRNA #300.
XX
XX Gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;
KW respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;
KW neotropic; uropathic; short interfering RNA; RNA interference; siRNA;
KW cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;
KW inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;
KW hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;
KW incontinence; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key misc_difference 13..14
FT misc_difference 13..14
FT //tag= a
FT //note= "deoxythymidine nucleotide"
XX
XX US2005014172-A1.
XX
XX 20-JAN-2005.
XX
XX 11-MAR-2004; 2004US-00798090.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 20-MAY-2002; 2002WO-US015876.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX 20-FEB-2003; 2003WO-US005028.
XX 20-FEB-2003; 2003WO-US005346.
XX 30-APR-2003; 2003US-00427160.
XX 23-MAY-2003; 2003US-0044853P.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 14-JAN-2004; 2004US-00757803.
XX
XX (RICH/) RICHARDS I.
PA (MCSW/) MCSWIGGEN J.
XX

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PI Richards I, Mcswiggen J;
XX WPI; 2005-090672/10.
XX
XX Novel chemically synthesized double stranded short interfering nucleic
XX acid molecule that directs cleavage of cholinergic receptor muscarinic 3
XX RNA through RNA interference, useful for treating asthma.
XX
XX Disclosure; SEQ ID NO 309; 84pp; English.
XX
XX The invention relates to a chemically synthesized double stranded short
XX interfering nucleic acid (siNA) molecule (I) that directs cleavage of a
XX cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,
XX where each strand of (I) has 19-23 nucleotides, and does not require the
XX presence of nucleotides having a 2-hydroxy group for mediating RNA
XX interference. (I) is useful for treating diseases e.g., asthma, allergic
XX rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary
XX vasoconstriction or hypertension, emphysema, irritable bowel syndrome,
XX Alzheimer's disease or urinary incontinence. (I) has increased resistance
XX towards nuclease. Double stranded short interfering nucleic acid molecule
XX was produced by solid phase oligonucleotide synthesis method. This
XX sequence represents an example of a siRNA molecule of the invention.
XX
SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 14; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14
DB 1 AUAUAUCUAUUUCG 14

RESULT 5
ADW27999
ID ADW27999 standard; RNA; 14 BP.
XX
XX AC ADW27999;
XX
XX 07-APR-2005 (first entry)
XX
XX Cholinergic receptor muscarinic 3 gene targeted siRNA #296.
XX
XX Gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;
KW respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;
KW neotropic; uropathic; short interfering RNA; RNA interference; siRNA;
KW cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;
KW inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;
KW hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;
KW incontinence; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key misc_difference 13..14
FT misc_difference 13..14
FT //tag= a
FT //note= "deoxythymidine nucleotide"
XX
XX US2005014172-A1.
XX
XX 20-JAN-2005.
XX
XX 11-MAR-2004; 2004US-00798090.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 20-MAY-2002; 2002WO-US015876.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX 20-FEB-2003; 2003WO-US005028.
XX 20-FEB-2003; 2003WO-US005346.
XX 30-APR-2003; 2003US-00427160.
XX 23-MAY-2003; 2003US-0044853P.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 14-JAN-2004; 2004US-00757803.
XX
XX (RICH/) RICHARDS I.
PA (MCSW/) MCSWIGGEN J.
XX

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PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 14-JAN-2004; 2004US-00757803.
XX
XX (RICH/) RICHARDS I.
XX (MCSW/) MCSWIGGEN J.
XX
XX Richards I, Mcswiggen J;
XX
XX WPI; 2005-090672/10.
XX
XX Novel chemically synthesized double stranded short interfering nucleic
XX acid molecule that directs cleavage of cholinergic receptor muscarinic 3
XX RNA through RNA interference, useful for treating asthma.
XX
XX Disclosure; SEQ ID NO 305; 84pp; English.
XX
XX The invention relates to a chemically synthesized double stranded short
XX interfering nucleic acid (siNA) molecule (I) that directs cleavage of a
XX cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,
XX where each strand of (I) has 19-23 nucleotides, and does not require the
XX presence of nucleotides having a 2-hydroxy group for mediating RNA
XX interference. (I) is useful for treating diseases e.g., asthma, allergic
XX rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary
XX vasoconstriction or hypertension, emphysema, irritable bowel syndrome,
XX Alzheimer's disease or urinary incontinence. (I) has increased resistance
XX towards nucleases. Double stranded short interfering nucleic acid molecule
XX was produced by solid phase oligonucleotide synthesis method. This
XX sequence represents an example of a siRNA molecule of the invention.
XX
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AUAUAUCUAUUUCG 14
XX |||||
XX Db 1 AUAUAUCUAUUUCG 14
XX
XX RESULT 6
XX ADW28009
XX ID ADW28009 standard; RNA; 14 BP.
XX
XX AC ADW28009;
XX
XX DT 07-APR-2005 (first entry)
XX
XX Cholinergic receptor muscarinic 3 gene targeted siRNA #306.
XX
XX gene expression; antiasthmatic; antiallergic; antiinflammatory; CNS-Gen.;
XX respiratory-gen.; hypotensive; gastrointestinal-gen.; neuroprotective;
XX neurotropic; uropathic; short interfering RNA; RNA interference; siRNA;
XX cholinergic receptor muscarinic 3; asthma; allergic rhinitis; sinusitis;
XX inflammation; allergy; cystic fibrosis; pulmonary vasoconstriction;
XX hypertension; emphysema; irritable bowel syndrome; Alzheimers disease;
XX incontinence; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH misc_difference 13..14
XX FT /*tag= a
XX FT /note= "deoxythymidine nucleotide"
XX
XX US2005014172-A1.
XX
XX 20-JAN-2005.

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XX 11-MAR-2004; 2004US-00798090.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 20-MAY-2002; 2002WO-US015876.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 09-SEP-2002; 2002US-0408378P.
XX 15-JAN-2003; 2003US-0409293P.
XX 20-FEB-2003; 2003WO-US005028.
XX 30-APR-2003; 2003US-00427160.
XX 23-MAY-2003; 2003US-00444853.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 14-JAN-2004; 2004US-00757803.
XX
XX (RICH/) RICHARDS I.
XX (MCSW/) MCSWIGGEN J.
XX
XX Richards I, Mcswiggen J;
XX
XX WPI; 2005-090672/10.
XX
XX Novel chemically synthesized double stranded short interfering nucleic
XX acid molecule that directs cleavage of cholinergic receptor muscarinic 3
XX RNA through RNA interference, useful for treating asthma.
XX
XX Disclosure; SEQ ID NO 315; 84pp; English.
XX
XX The invention relates to a chemically synthesized double stranded short
XX interfering nucleic acid (siNA) molecule (I) that directs cleavage of a
XX cholinergic receptor muscarinic 3 (CHRM3) RNA through RNA interference,
XX where each strand of (I) has 19-23 nucleotides, and does not require the
XX presence of nucleotides having a 2-hydroxy group for mediating RNA
XX interference. (I) is useful for treating diseases e.g., asthma, allergic
XX rhinitis, sinusitis, inflammation, allergy, cystic fibrosis, pulmonary
XX vasoconstriction or hypertension, emphysema, irritable bowel syndrome,
XX Alzheimer's disease or urinary incontinence. (I) has increased resistance
XX towards nucleases. Double stranded short interfering nucleic acid molecule
XX was produced by solid phase oligonucleotide synthesis method. This
XX sequence represents an example of a siRNA molecule of the invention.
XX
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AUAUAUCUAUUUCG 14
XX |||||
XX Db 1 AUAUAUCUAUUUCG 14
XX
XX RESULT 7
XX ADW73595
XX ID ADW73595 standard; RNA; 14 BP.
XX
XX AC ADW73595;
XX
XX DT 07-APR-2005 (first entry)
XX
XX Human B7-H1 siRNA target sequence oligonucleotide SeqID295.
XX
XX short interfering RNA; RNA interference; gene silencing; siRNA; B7-H1;
XX cytostatic; vasotropic; nephrotropic; immunomodulator; tumor;
XX immune disorder; proliferative disorder; cancer; restenosis;
XX renal disease; ss.
XX
XX Homo sapiens.
XX

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PN WO2005007855-A2.  
 XX 27-JAN-2005.  
 PD 14-JUL-2004; 2004WO-US022658.  
 XX 14-JUL-2003; 2003US-0487214P.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Usman N, Mcswiggen J;  
 PI WPI; 2005-112870/12.  
 DR New double stranded short interfering nucleic acid molecule that directs  
 XX cleavage of a B7-H1 RNA, useful for treating tumor-mediated  
 XX immunosuppression, immunopathology and/or proliferative diseases, cancer,  
 XX or restenosis.  
 PS Disclosure; SEQ ID NO 295; 191pp; English.  
 XX This invention relates to a novel chemically synthesized double stranded  
 XX short interfering nucleic acid (siRNA) molecule that directs cleavage of  
 CC a B7-H1 RNA via RNA interference (RNAi), where each strand of the siRNA  
 CC molecule is 18-23 nucleotides in length, and one strand of the siRNA  
 CC molecule comprises nucleotide sequence is complementary to the B7-H1 RNA  
 CC for the siRNA molecule to direct cleavage of the B7-H1 RNA via RNA  
 CC interference. The invention may be useful for the production of compounds  
 CC with a cytostatic, vasotropic, nephrotropic or immunomodulator through  
 CC RNA interference. The siRNA, compounds, compositions, and methods are  
 CC useful for modulating B7-H1 gene expression and for treating tumor-  
 CC mediated immunosuppression, immunopathology and/or proliferative diseases  
 CC and conditions like cancer, restenosis or polycystic kidney disease. The  
 CC present sequence is that of a region of the human B7-H1 which was  
 CC targeted by an siRNA oligonucleotide of the invention.  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 SQ Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AUAUAUCUAUUUCG 14  
 DB 1 AUAUAUCUAUUUCG 14  
 RESULT 8  
 ADV94764  
 ID ADV94764 standard; RNA; 14 BP.  
 XX ADV94764;  
 AC 07-APR-2005 (first entry)  
 XX Human short interfering nucleic acid SEQ ID NO 1901.  
 DE nototropic; neuroprotective; cerebroprotective; vasotropic;  
 XX cardiovascular-gen.; gene expression; dementia; degeneration;  
 KW Alzheimer's disease; neurodegenerative disease; neurological disease;  
 KW cerebrovascular ischemia; short interfering RNA; siRNA; RNA interference;  
 KW gene silencing; ss.  
 XX Homo sapiens.  
 OS

OS Synthetic.  
 XX WO2005003350-A2.  
 PN 13-JAN-2005.  
 PD 25-JUN-2004; 2004WO-US020516.  
 XX 27-JUN-2003; 2003US-00607933.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L;  
 PI WPI; 2005-091819/10.  
 DR New chemically synthesized double stranded short interfering nucleic acid  
 XX (siRNA) molecule that directs cleavage of an amyloid precursor protein  
 XX (APP) RNA via RNA interference (RNAi), useful for treating Alzheimer's  
 XX disease.  
 PS Disclosure; SEQ ID NO 1901; 233pp; English.  
 XX The invention describes a chemically synthesized double stranded short  
 XX interfering nucleic acid (siRNA) molecule that directs cleavage of an  
 CC amyloid precursor protein (APP) RNA via RNA interference (RNAi). Each  
 CC strand of the siRNA molecule 18-20 nucleotides in length, and one strand  
 CC of the siRNA molecule comprises nucleotide sequence having sufficient  
 CC complementarity to the APP RNA for the siRNA molecule to direct cleavage  
 CC of the APP RNA via RNA interference. Also described is a composition  
 CC comprising the siRNA molecule in a pharmaceutically acceptable carrier or  
 CC diluent. Also disclosed are siRNAs for modulating the expression of other  
 CC genes implicated in Alzheimer's disease and/or dementia, especially beta-  
 CC secretase (BACE), Pin-1, presenilin 1 or presenilin 2. The molecules  
 CC and composition are useful for treating Alzheimer's disease,  
 CC neurodegenerative disorders or conditions, and stroke/cardiovascular  
 CC accident in a subject. This sequence represents a short interfering  
 CC nucleic acid (siRNA) used to demonstrate the creation of siRNA's used in  
 CC the invention.  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 SQ Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AUAUAUCUAUUUCG 14  
 DB 1 AUAUAUCUAUUUCG 14  
 RESULT 9  
 ADV79835  
 ID ADV79835 standard; RNA; 14 BP.  
 XX ADV79835;  
 AC 07-APR-2005 (first entry)  
 XX Exemplary duplex forming RNA oligo, SEQ ID 952.  
 DE short interfering RNA; siRNA; gene silencing; RNA interference;  
 XX anorectic; cardiant; cardiovascular-gen.; antidiabetic; gene therapy;  
 KW obesity; coronary disease; cardiovascular disease; insulin resistance;  
 KW

KW mitochondria; ss.  
XX  
OS Synthetic.  
XX  
PN WO2005007859-A2.  
XX  
PD 27-JAN-2005.  
XX  
XX  
XX 09-JUL-2004; 2004WO-US022247.  
XX  
XX 11-JUL-2003; 2003US-0486729P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX  
XX Mcswiggen J, Usman N;  
PI  
XX  
XX WPI; 2005-112874/12.  
XX  
XX  
XX New chemically synthesized double stranded short interfering nucleic acid  
PT molecule directing cleavage of acetyl-CoA carboxylase RNA through RNA  
PT interference, useful for treating obesity, cardiovascular disease,  
PT insulin resistance.  
XX  
XX Disclosure; SEQ ID NO 952; 200pp; English.  
XX  
XX The invention relates to a novel, chemically synthesized double stranded  
CC short interfering nucleic acid (siNA) molecule directing cleavage of  
CC acetyl-CoA carboxylase RNA through RNA interference. Each strand of the  
CC siNA molecule is 18-23 nucleotides in length, and one strand has  
CC sufficient nucleotide sequence complementarity to acetyl-CoA carboxylase  
CC RNA for the siNA to direct cleavage of the acetyl-CoA carboxylase RNA  
CC through RNA interference. The invention further comprises: a composition  
CC comprising the siNA and a carrier and diluent; increasing the stability  
CC of an siNA molecule; modulating the expression of acetyl CoA carboxylase  
CC gene within a cell; an expression vector encoding siNA; synthesizing an siNA;  
CC and a method for screening chemically modified siNA molecules that are  
CC active in mediating RNA interference against a target nucleic acid  
CC sequence (sequence of acetyl CoA carboxylase gene). The siNA molecules  
CC have anorectic, cardiant, cardiovascular-gen., and antidiabetic  
CC activities. The siNA molecules may be used in gene therapy. The siNA  
CC molecules are useful for modulating the expression of acetyl-CoA  
CC carboxylase genes associated with the development of obesity,  
CC coronary/cardiovascular disease, insulin resistance and/or mitochondrial  
CC disease. The siNA molecules are useful in therapeutic, diagnostic, target  
CC validation, genomic discovery, genetic engineering, and pharmacogenomic  
CC applications. The siNA molecules and compositions are useful for treating  
CC obesity, coronary/cardiovascular disease, insulin resistance and/or  
CC mitochondrial disease. This polynucleotide sequence represents a duplex  
CC forming RNA oligo used in the exemplification of the invention.  
XX  
XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
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XX Query Match 100.0%; Score 14; DB 14; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AUAUAUCUAUUUCG 14  
DB 1 AUAUAUCUAUUUCG 14  
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|||||  
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ADW79836/c  
ID ADW79836 standard; RNA; 14 BP.

XX  
AC ADM79836;  
XX  
XX 07-APR-2005 (first entry)  
XX  
XX Exemplary duplex forming RNA oligo, SEQ ID 953.  
XX  
XX short interfering RNA; siRNA; gene silencing; RNA interference;  
KW anorectic; cardiant; cardiovascular-gen.; antidiabetic; gene therapy;  
KW obesity; coronary disease; cardiovascular disease; insulin resistance;  
KW mitochondria; ss.  
XX  
XX Synthetic.  
XX  
XX WO2005007859-A2.  
XX  
XX 27-JAN-2005.  
XX  
XX 09-JUL-2004; 2004WO-US022247.  
XX  
XX 11-JUL-2003; 2003US-0486729P.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX  
XX Mcswiggen J, Usman N;  
PI  
XX  
XX WPI; 2005-112874/12.  
XX  
XX  
XX New chemically synthesized double stranded short interfering nucleic acid  
PT molecule directing cleavage of acetyl-CoA carboxylase RNA through RNA  
PT interference, useful for treating obesity, cardiovascular disease,  
PT insulin resistance.  
XX  
XX Disclosure; SEQ ID NO 953; 200pp; English.  
XX  
XX The invention relates to a novel, chemically synthesized double stranded  
CC short interfering nucleic acid (siNA) molecule directing cleavage of  
CC acetyl-CoA carboxylase RNA through RNA interference. Each strand of the  
CC siNA molecule is 18-23 nucleotides in length, and one strand has  
CC sufficient nucleotide sequence complementarity to acetyl-CoA carboxylase  
CC RNA for the siNA to direct cleavage of the acetyl-CoA carboxylase RNA  
CC through RNA interference. The invention further comprises: a composition  
CC comprising the siNA and a carrier and diluent; increasing the stability  
CC of an siNA molecule; modulating the expression of acetyl CoA carboxylase  
CC gene within a cell; an expression vector encoding siNA; synthesizing an siNA;  
CC comprising the vector; a kit comprising the siNA; synthesizing an siNA;  
CC and a method for screening chemically modified siNA molecules that are  
CC active in mediating RNA interference against a target nucleic acid  
CC sequence (sequence of acetyl CoA carboxylase gene). The siNA molecules  
CC have anorectic, cardiant, cardiovascular-gen., and antidiabetic  
CC activities. The siNA molecules may be used in gene therapy. The siNA  
CC molecules are useful for modulating the expression of acetyl-CoA  
CC carboxylase genes associated with the development of obesity,  
CC coronary/cardiovascular disease, insulin resistance and/or mitochondrial  
CC disease. The siNA molecules are useful in therapeutic, diagnostic, target  
CC validation, genomic discovery, genetic engineering, and pharmacogenomic  
CC applications. The siNA molecules and compositions are useful for treating  
CC obesity, coronary/cardiovascular disease, insulin resistance and/or  
CC mitochondrial disease. This polynucleotide sequence represents a duplex  
CC forming RNA oligo used in the exemplification of the invention.  
XX  
XX Sequence 14 BP; 7 A; 1 C; 2 G; 0 T; 4 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 14; DB 14; Length 14;  
XX Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AUAUAUCUAUUUCG 14  
DB 1 AUAUAUCUAUUUCG 14  
|||||  
|||||  
Query Match 100.0%; Score 14; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;



CC a two nucleotide 3' overhang, or can also form a stem loop construct.  
 XX  
 SQ Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
 Query Match 100.0%; Score 14; DB 14; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
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 QY 1 AUAUAUCUAUUUCG 14  
 |||||  
 Db 1 AUAUAUCUAUUUCG 14  
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 ADX87169  
 ID ADX87169 standard; RNA; 14 BP.  
 XX  
 AC ADX87169;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE XIAP targeting siRNA SEQ ID NO 1057.  
 XX  
 KW ds; primer; short interfering RNA; siRNA;  
 KW X-linked inhibitor of apoptosis protein; XIAP; RNA interference; RNAi;  
 KW cytoskeletal; cancer; gene silencing.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005014811-A2.  
 XX  
 PD 17-FEB-2005.  
 XX  
 XX 06-AUG-2004; 2004WO-US025589.  
 XX  
 PR 08-AUG-2003; 2003US-0493561P.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 30-APR-2004; 2004WO-US013456.  
 PR 24-MAY-2004; 2004WO-US016390.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 XX McSwiggen J, Chowrira BM;  
 PI WPI; 2005-163247/17.  
 DR  
 XX  
 XX New chemically synthesized double stranded short interfering nucleic acid  
 PT that directs cleavage of an X-linked inhibitor of apoptosis protein  
 PT (XIAP) RNA via RNA interference, useful in preparing a composition for  
 PT treating cancer.  
 XX  
 XX Claim 33; SEQ ID NO 1057; 202pp; English.  
 PS  
 XX  
 XX This invention describes novel chemically synthesized double stranded  
 CC short interfering nucleic acid (siRNA) molecules which direct cleavage of  
 CC a X-linked inhibitor of apoptosis protein (XIAP) RNA via RNA interference  
 CC (RNAi), where each strand of the siRNA molecule is about 18-23  
 CC nucleotides in length and one strand of the siRNA molecule comprises  
 CC nucleotide sequence having sufficient complementarity to the XIAP RNA.  
 CC The siRNA molecules can be used to make a cytoskeletal composition  
 CC comprising the siRNA molecule in a carrier or diluent. The sense and  
 CC antisense strands are connected via a linker molecule. The pyrimidine  
 CC nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.  
 CC The purine nucleotides in the sense region are 2'-deoxy purine  
 CC nucleotides and the pyrimidine nucleotides are 2'-deoxy-2'-fluoro  
 CC pyrimidine nucleotides. The fragment comprising the sense region includes  
 CC a terminal cap moiety at a 5'-end, a 3'-end, or both of the 5' and 3'

CC ends of the fragment comprising the sense region. The terminal cap moiety  
 CC is an inverted deoxy abasic moiety. The pyrimidine nucleotides of the  
 CC antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the  
 CC purine nucleotides are 2'-O-methyl purine nucleotides. The purine  
 CC nucleotides present in the antisense region comprise 2'-deoxy- purine  
 CC nucleotides. The antisense region comprises a phosphorothioate  
 CC internucleotide linkage at the 3' end of the antisense region. The  
 CC antisense region comprises a glyceryl modification at a 3' end of the  
 CC antisense region. About 19 nucleotides of each fragment of the siRNA  
 CC molecule are base-paired to the complementary nucleotides of the other  
 CC fragment of the siRNA. The 5'-end of the fragment comprising the  
 CC antisense region optionally includes a phosphate group. The XIAP RNA  
 CC comprises Genbank Accession No. NM\_001167. The chemically synthesized  
 CC double stranded short interfering nucleic acid (siRNA) molecule is useful  
 CC in preparing a composition for treating cancer. ADX86130-ADX87180  
 CC represent siRNA molecules which are used in RNA interference mediated  
 CC inhibition of XIAP gene expression.  
 XX  
 XX Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other;  
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 ADY91198  
 ID ADY91198 standard; RNA; 14 BP.  
 XX  
 AC ADY91198;  
 XX  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE VEGF/VEGFR DFO siRNA SEQ ID NO 4249.  
 XX  
 KW ss; siRNA; short interfering RNA; RNA interference; gene silencing; VEGF;  
 KW pharmaceutical; cancer; neoplasm; Cytostatic; VEGFR.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005028649-A1.  
 XX  
 PD 31-MAR-2005.  
 XX  
 XX 16-SEP-2004; 2004WO-US030488.  
 XX  
 PR 16-SEP-2003; 2003US-00664767.  
 PR 16-SEP-2003; 2003US-00665255.  
 PR 23-SEP-2003; 2003US-00670011.  
 PR 23-OCT-2003; 2003US-00693059.  
 PR 24-NOV-2003; 2003US-00720448.  
 PR 03-DEC-2003; 2003US-00727780.  
 PR 14-JAN-2004; 2004US-00757803.  
 PR 26-JAN-2004; 2004US-00764957.  
 PR 10-FEB-2004; 2004US-0543480P.  
 PR 13-FEB-2004; 2004US-00780447.  
 PR 16-APR-2004; 2004US-00826966.  
 PR 23-APR-2004; 2004US-00831620.  
 PR 30-APR-2004; 2004US-00013456.  
 PR 11-MAY-2004; 2004US-00844076.  
 XX  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA  
 XX Jadhav V, Kossen K, Zinnen S, Vaish N, McSwiggen J;  
 PI WPI; 2005-254128/26.  
 XX  
 XX New multifunctional siNA molecule that directs cleavage of the first and  
 PT second VEGF or VEGFR target sequences via RNA interference, useful in

PT preparing a composition for treating cell proliferative disorders e.g.  
PT cancers.

PS Disclosure; SEQ ID NO 4249; 396pp; English.

The invention relates to a multifunctional siNA molecule comprising a structure having Formula MP-III and which directs cleavage of the first and second VEGF or VEGFR target sequences via RNA interference. The multifunctional siNA molecule is useful in preparing a pharmaceutical composition for treating cell proliferative disorders, e.g. cancer. The present sequence represents a VEGF/VEGFR DFO siRNA.

Sequence 14 BP; 4 A; 2 C; 1 G; 0 T; 7 U; 0 Other; 0 SQ

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Query Match      100.0%; Score 14; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0 Indels
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QY 1 AUAUAUCUAUUCG 14  
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pb 1 AUAUAUCUAUUCG 14

## RESULT 15

ADZ02756  
ID ADZ02756 standard; RNA; 14 BP.

ADZ02756;

16-JUN-2005 (first entry)

DE Hepatitis C virus short interfering nucleic acid SEQ ID NO 2028.

antiinflammatory; hepatotropic; virucide; gene therapy; RNA interference; gene silencing; antisense therapy; antisense oligonucleotide; pharmaceutical; gene expression; hepatitis C virus infection; gastrointestinal disease; infection; siRNA; short interfering RNA; ss...

Hepatitis C virus.

XX  
PN WO2005028650-A2.

31-MAR-2005

15-SEP-2004: 2004WO-US031012.

16-SEP-2003: 2003US-00667271

PR 23-OCT-2003; 2003US-00693059.

PR 24-NOV-2003; 2003US-00720448.

PR 03-DEC-2003; 2003US-00727780.

14 - JAN - 2004; 2004US-00757803.

PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447

PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.

30-APR-2004; 2004WO-US013456.  
PR

PR 24-MAY-2004; 2004WO-US016390.

XX

PA (SIRN-) SIRNA THERAPEUTICS INC.

PI Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;

DR WPI; 2005-254129/26.

PT New multifunctional siNA molecule that directs cleavage of the first and  
PT second hepatitis C virus (HCV) target sequences via RNA interference,  
PT useful in preparing a composition for treating hepatitis C virus (HCV)  
PT infection.

PS Disclosure; SEQ ID NO 2028; 300pp; English.

The invention describes a new multifunctional siNA molecule comprises a structure having Formula MF-III and directs cleavage of the first and second hepatitis C virus (HCV) target sequences via RNA interference.

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us-10-824-036a-3578.sz40.rn1

Thu Jun 29 15:49:22 2006

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2006, 23:25:11 ; Search time 97 Seconds  
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Perfect score: 14  
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Scoring table: IDENTITY\_NUC  
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Total number of hits satisfying chosen parameters: 1304306

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Maximum DB seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*  
4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*  
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6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*  
7: /EMC Celerra\_SIDS3/ptodata/2/ina/PCTUS COMB.seq.\*  
8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*  
9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*  
10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	12.4	88.6	24	3	US-09-392-486-1
C 2	12	85.7	36	3	US-09-735-271-1975
C 3	12	85.7	38	5	US-10-156-306B-1236
C 4	12	85.7	39	2	US-08-369-829A-11
C 5	12	85.7	39	2	US-08-586-676E-15
C 6	11.4	81.4	20	3	US-10-177-573-44
C 7	11.4	81.4	25	3	US-09-396-196G-40617
C 8	11.4	81.4	26	3	US-09-814-134A-7
C 9	11.4	81.4	33	3	US-08-817-926-38
C 10	11.4	81.4	33	3	US-09-297-053-5
C 11	11	78.6	24	3	US-08-262-220-2
C 12	11	78.6	24	3	US-08-471-733-2
C 13	11	78.6	24	3	US-08-468-878-2
C 14	11	78.6	24	3	US-08-750-494-2
C 15	11	78.6	24	3	US-08-470-638-2
C 16	11	78.6	25	2	US-08-257-781-15
C 17	11	78.6	25	3	US-09-396-196G-24676
C 18	11	78.6	25	7	PCT-US95-06857-15
C 19	11	78.6	34	3	US-09-565-808-6
C 20	11	78.6	36	2	US-08-585-684B-596
C 21	11	78.6	36	3	US-09-038-073-596
C 22	11	78.6	38	5	US-10-156-306B-5493
C 23	10.8	77.1	16	2	US-08-192-941-8

24	10.8	77.1	19	3	US-08-850-961-25	Sequence 25, Appl
25	10.8	77.1	19	3	US-09-479-776-25	Sequence 25, Appl
26	10.8	77.1	20	3	US-09-418-980-24	Sequence 24, Appl
27	10.8	77.1	21	2	US-08-184-941-8	Sequence 8, Appl
28	10.8	77.1	22	3	US-08-850-961-4	Sequence 4, Appl
29	10.8	77.1	22	3	US-09-479-776-4	Sequence 4, Appl
C 30	10.8	77.1	25	3	US-08-396-196G-69848	Sequence 69848, A
C 31	10.8	77.1	30	3	US-09-027-169-11	Sequence 11, Appl
C 32	10.8	77.1	33	3	US-09-417-197-33	Sequence 33, Appl
C 33	10.8	77.1	36	2	US-08-809-458B-1	Sequence 9, Appl
C 34	10.8	77.1	38	2	US-07-805-564A-9	Sequence 9, Appl
C 35	10.8	77.1	38	2	US-08-114-301-9	Sequence 7, Appl
C 36	10.8	77.1	38	7	PCT-US92-10431-9	Sequence 55, Appl
C 37	10.8	77.1	40	2	US-08-425-684-7	Sequence 7, Appl
C 38	10.8	77.1	40	2	US-08-675-502-7	Sequence 55, Appl
C 39	10.8	77.1	40	2	US-08-675-502-55	Sequence 7, Appl
C 40	10.8	77.1	40	3	US-09-245-802-7	Sequence 55, Appl
C 41	10.8	77.1	40	3	US-09-245-802-55	Sequence 42, Appl
C 42	10.8	77.1	40	3	US-09-245-802-55	Sequence 489, App
C 43	10.6	75.7	21	7	PCT-US91-03680-42	Sequence 490, App
C 44	10.4	74.3	16	3	US-09-479-005A-489	
C 45	10.4	74.3	16	3	US-09-479-005A-490	

## ALIGNMENTS

RESULT 1  
US-09-392-486-1/c  
; Sequence 1, Application US/09392486  
; Patent No. 6255054  
; GENERAL INFORMATION:  
; APPLICANT: HUGON, Jacques  
; APPLICANT: BACLET, Marie-Claire  
; TITLE OF INVENTION: POLYMORPHISM OF THE HUMAN GluR-5 GENE AND RISK FACTOR  
; FILE REFERENCE: R-340205  
; CURRENT APPLICATION NUMBER: US/09/392,486  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.2  
; SEQ ID NO 1  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer derived from Human glutamate (Kainate) receptor 5 (GluR-5)  
US-09-392-486-1

Query Match 88.6%; Score 12.4; DB 3; Length 24;  
Best Local Similarity 42.9%; Pred. No. 4.6e+03;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 AUAUACUUAUUCG 14  
Db 15 ATATATCTATTAG 2  
|:|:|:|:|:|:|

RESULT 2  
US-09-735-271-1975  
; Sequence 1975, Application US/09735271  
; Patent No. 6869762  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Mark J.  
; APPLICANT: Hudson, Thomas J.  
; APPLICANT: Landier, Eric S.  
; APPLICANT: Rioux, John  
; APPLICANT: Siminovich, Kathy  
; TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS  
; FILE REFERENCE: 2825.1025-002  
; CURRENT APPLICATION NUMBER: US/09/735,271  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 60/170,257

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; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/196,046
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2058
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1975
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1975

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Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

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Db 10 ATATCTATTTC 22

RESULT 3
US-10-156-306B-1236/c
; Sequence 1236, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1236
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306B-1236

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Best Local Similarity 50.0%; Pred. No. 7e+03;
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Db 38 ATATCTATTTC 27

RESULT 4
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; Sequence 11, Application US/08369829A
; Patent No. 5861377
; GENERAL INFORMATION:
; APPLICANT: Hans Fritz
; APPLICANT: Christian Sommerhoff
; APPLICANT: Jutta Heim
; TITLE OF INVENTION: No. 5861377el Inhibitor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5861377artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07936
; COMPUTER READABLE FORM:

Query Match      85.7%; Score 12; DB 5; Length 38;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 AUAUACUUAUUC 14
Db 38 ATATCTATTTC 27

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US-08-369-829A-11
; Sequence 11, Application US/08369829A
; Patent No. 5861377
; GENERAL INFORMATION:
; APPLICANT: Hans Fritz
; APPLICANT: Christian Sommerhoff
; APPLICANT: Jutta Heim
; TITLE OF INVENTION: No. 5861377el Inhibitor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5861377artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07936
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/369,829A
; FILING DATE: 6-JAN-95
; PRIOR APPLICATION DATA: EPO 94810006.0
; APPLICATION NUMBER: 7-JAN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5861377ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-19942/A/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..39
; OTHER INFORMATION: /function= "synthetic oligo for PCR"
US-08-369-829A-11

Query Match      85.7%; Score 12; DB 2; Length 39;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 AUAUACUUAUUC 14
Db 28 ATATCTATTTC 39

RESULT 5
US-08-586-676B-15
; Sequence 15, Application US/08586676E
; Patent No. 5972698
; GENERAL INFORMATION:
; APPLICANT: Fritz, Hans,
; APPLICANT: Sommerhoff, Christian
; TITLE OF INVENTION: Tryptase inhibitor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5972698artis Corporation, Patent and Trademark Department
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07901-1027
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,676E
; FILING DATE: 25-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02445
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111930.9
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Heena J.
; REGISTRATION NUMBER: 22,640
; REFERENCE/DOCKET NUMBER: 4-20076/PCT
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 522 6940  
TELEFAX: (908) 522 6955  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: synthetic DNA  
US-08-586-676E-15

Query Match 85.7%; Score 12; DB 2; Length 39;  
Best Local Similarity 50.0%; Pred. No. 7e+03;  
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 AUAUCUAUUCG 14  
|:|:|:|:|:  
Db 28 ATATCTATTTCG 39

RESULT 6  
US-10-177-573-44  
Sequence 44, Application US/10177573  
Patent No. 6828149  
GENERAL INFORMATION:  
APPLICANT: Susan M. Freier  
TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3R1 EXPRESSION  
FILE REFERENCE: RTS-0364  
CURRENT APPLICATION NUMBER: US/10/177,573  
CURRENT FILING DATE: 2002-06-20  
NUMBER OF SEQ ID NOS: 104  
SEQ ID NO 44  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense oligonucleotide  
US-10-177-573-44

Query Match 81.4%; Score 11.4; DB 3; Length 20;  
Best Local Similarity 46.2%; Pred. No. 1.4e+04;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:  
Db 2 ATATATCTATTAC 14

RESULT 7  
US-09-396-196G-40617  
Sequence 40617, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittmann  
APPLICANT: David Meck  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100, 678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 40617  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-40617

Query Match 81.4%; Score 11.4; DB 3; Length 25;

Best Local Similarity 38.5%; Pred. No. 1.4e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:  
Db 1 ATTATCTATTTC 13

RESULT 8  
US-09-814-134A-7/c  
Sequence 7, Application US/09814134A  
Patent No. 6395531  
GENERAL INFORMATION:  
APPLICANT: Kong, Huimin  
APPLICANT: Higgins, Lauren Sears  
TITLE OF INVENTION: Method For Cloning And Expression of MlyI Restriction  
TITLE OF INVENTION: Endonuclease And MlyI Methylase And BstNBII Methylase  
TITLE OF INVENTION: in E. coli  
FILE REFERENCE: NEB-186  
CURRENT APPLICATION NUMBER: US/09/814,134A  
CURRENT FILING DATE: 2001-03-21  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Micrococcus lylae  
US-09-814-134A-7

Query Match 81.4%; Score 11.4; DB 3; Length 26;  
Best Local Similarity 46.2%; Pred. No. 1.4e+04;  
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUAUUC 13  
|:|:|:|:|:  
Db 24 ATATATCTAATTC 12

RESULT 9  
US-08-817-926-38/c  
Sequence 38, Application US/08817926  
Patent No. 6001590  
GENERAL INFORMATION:  
APPLICANT: Kameda, Toshihiro  
APPLICANT: Suda, Hisako  
APPLICANT: Tamai, Yukio  
APPLICANT: Iwamatsu, Akihiro  
APPLICANT: Kato, No. 6001590uo  
APPLICANT: Sakai, Yasuyoshi  
TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINI  
TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,926  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/02597  
FILING DATE: 12-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 234133/1995

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; FILING DATE: 12-SEP-1995
; PRIOR APPLICATION DATA: JP 42536/1996
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 081356/0112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
;
US-08-817-926-38

Query Match      81.4%; Score 11.4; DB 3; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 22 ATGTATCTATTTC 10

RESULT 10
US-09-297-053-5/c
; Sequence 5, Application US/09297053
; Patent No. 6274340
; GENERAL INFORMATION:
; APPLICANT: KOMEDA, Toshihiro
; TITLE OF INVENTION: DNA SEQUENCE INCREASING PROMOTER ACTIVITY
; FILE REFERENCE: 081356/0131
; CURRENT APPLICATION NUMBER: US/09/297,053
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: PCT/JP98/03848
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: JP 9-234995
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
;
US-09-297-053-5

Query Match      81.4%; Score 11.4; DB 3; Length 33;
Best Local Similarity 38.5%; Pred. No. 1.4e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 22 ATGTATCTATTTC 10

RESULT 11
US-08-262-220-2/c
; Sequence 2, Application US/08262220
; Patent No. 6054296
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
```

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,220
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-262-220-2

Query Match      78.6%; Score 11; DB 3; Length 24;
Best Local Similarity 38.5%; Pred. No. 2.2e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUC 13
Db 13 AWATATCTTTTC 1

RESULT 12
US-08-471-733-2/c
; Sequence 2, Application US/08471733
; Patent No. 6068842
; GENERAL INFORMATION:
; APPLICANT: BERGSTROM SVEN
; APPLICANT: BARBOUR ALAN G.
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 SEVENTH STREET, N.W.
; CITY: WASHINGTON
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,733
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM-3
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-471-733-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

## RESULT 13

US-08-468-878-2/c  
Sequence 2, Application US/08468878  
Patent No. 6090586  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,878  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/262,220  
FILING DATE: 20-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: BERGSTROM=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-468-878-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

## RESULT 14

US-08-750-494-2/c  
Sequence 2, Application US/08750494  
Patent No. 6204018  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/750,494  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/262,220  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: COOPER, IVER P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: BERGSTROM=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-750-494-2

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13  
Db 13 AWATATCTTTTC 1

## RESULT 15

US-08-470-638-2/c  
Sequence 2, Application US/08470638  
Patent No. 6509017  
GENERAL INFORMATION:  
APPLICANT: BERGSTROM SVEN  
APPLICANT: BARBOUR ALAN G.  
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 SEVENTH STREET, N.W.  
CITY: WASHINGTON  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 78.6%; Score 11; DB 3; Length 24;  
Best Local Similarity 38.5%; Pred. No. 2.2e+04;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,638
; FILING DATE: 06-06-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/262,220
; FILING DATE: 20-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: BERGSTROM=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-470-638-2
;
Query Match          78.6%; Score 11; DB 3; Length 24;
Best Local Similarity 38.5%; Pred. No. 2.2e+04;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
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QY      1 AUUAUUAUUUC 13
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Db      13 AWATATCTTTTC 1
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Search completed: June 28, 2006, 23:31:41  
Job time : 97 secs

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions `.napbm` (Published Applications NA Main) and `.rnppbm` (Published Applications NA New).  
Searches run against Amino Acid Published Applications produce two sets of results, with the extensions `.rapbm` (Published Applications AA Main) and `.rnppbm` (Published Applications AA New).

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: June 28, 2006, 23:30:19 ; Search time 818 Seconds  
(without alignments)  
210.302 Million cell updates/sec  
Title: US-10-824-036A-3578  
Perfect score: 14  
Sequence: 1 auaaucauuuucg 14  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 18992170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 23675114  
Minimum DB seq length: 0  
Maximum DB seq length: 40  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications NA Main:  
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2: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
3: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
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7: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
8: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
9: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
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12: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
13: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
14: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11B\_PUBCOMB.seq.\*  
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16: /EMC\_Celerra\_SID33/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	9	US-10-820-622-73
2	14	100.0	14	9	US-10-820-622-74
3	14	100.0	14	10	US-10-894-475-419
4	14	100.0	14	10	US-10-923-115-355
5	14	100.0	14	10	US-10-869-638-467
6	14	100.0	14	10	US-10-871-222-703
7	14	100.0	14	10	US-10-879-867-437
8	14	100.0	14	10	US-10-883-218-927
9	14	100.0	14	10	US-10-888-226-952
10	14	100.0	14	10	US-10-892-922-293
11	14	100.0	14	10	US-10-881-118-449
12	14	100.0	14	10	US-10-861-060-371
13	14	100.0	14	10	US-10-863-973-1829
14	14	100.0	14	10	US-10-922-544-471
15	14	100.0	14	10	US-10-923-330-765
16	14	100.0	14	10	US-10-916-095-187
17	14	100.0	14	10	US-10-916-095-188

ALIGNMENTS

RESULT 1  
US-10-820-622-73  
; Sequence 73, Application US/10820622  
; Publication No. US20050042632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sarna Therapeutics, Inc.  
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids  
; FILE REFERENCE: 900/051 (MBH02-030-B)  
; CURRENT APPLICATION NUMBER: US/10/820,622  
; CURRENT FILING DATE: 2004-04-08  
; PRIOR APPLICATION NUMBER: US 10/366,191  
; PRIOR FILING DATE: 2003-02-12  
; PRIOR APPLICATION NUMBER: US 60/356,298  
; PRIOR FILING DATE: 2002-02-13  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: s1NA target region  
US-10-820-622-73

Query Match 100.0%; Score 14; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AUAUAUCUAUUUCG 14  
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Db 1 AUAUAUCUAUUUCG 14

RESULT 2  
US-10-820-622-74/c  
; Sequence 74, Application US/10820622  
; Publication No. US20050042632A1  
; GENERAL INFORMATION:  
; APPLICANT: Sarna Therapeutics, Inc.

Sequence 715, App  
Sequence 683, App  
Sequence 381, App  
Sequence 683, App  
Sequence 684, App  
Sequence 1691, App  
Sequence 1692, App  
Sequence 421, App  
Sequence 421, App  
Sequence 677, App  
Sequence 678, App  
Sequence 301, App  
Sequence 747, App  
Sequence 748, App  
Sequence 2752, App  
Sequence 323, App  
Sequence 1360, App  
Sequence 1461, App  
Sequence 879, App  
Sequence 880, App  
Sequence 195, App  
Sequence 321, App  
Sequence 322, App  
Sequence 1139, App  
Sequence 1140, App  
Sequence 807, App  
Sequence 808, App  
Sequence 301, App

14 100.0 14 10 US-10-844-072-715  
14 100.0 14 10 US-10-915-896-683  
14 100.0 14 10 US-10-916-030-381  
14 100.0 14 10 US-10-922-626-683  
14 100.0 14 10 US-10-922-626-684  
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14 100.0 14 10 US-10-922-340-747  
14 100.0 14 10 US-10-922-340-748  
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14 100.0 14 10 US-10-923-182-808  
14 100.0 14 10 US-10-903-128-301

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43 14 100.0 14 10  
44 14 100.0 14 10  
45 14 100.0 14 10

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; APPLICANT: Susan, Radka
; TITLE OF INVENTION: Antibodies Having Specificity for Nucleic Acids
; FILE REFERENCE: 900/051 (MBHB02-030-B)
; CURRENT APPLICATION NUMBER: US/10/820,622
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 10/366,191
; PRIOR FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 60/356,298
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA complementary region
US-10-820-622-74

Query Match      100.0%; Score 14; DB 9; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
      |||:|:|:|:|:|
Db      14 ATATATCTATTTCG 1

RESULT 3
US-10-894-475-419
; Sequence 419, Application US/10894475
; Publication No. US20050070497A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine
; TITLE OF INVENTION: Phosphatase-1B (PTP-1B) Gene Expression Using Short Interfering
; FILE REFERENCE: 02-738-F (400/169)
; CURRENT APPLICATION NUMBER: US/10/894,475
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US 03/04123
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 10/206,705
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 355
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-923-115-355

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
      |||:|:|:|:|:|
Db      1 AUAUAUCUAUUUCG 14

RESULT 4
US-10-923-115-355
; Sequence 355, Application US/10923115
; Publication No. US20050079610A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Polisky, Barry
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of FOS Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/193 (MBHB03-194-A)
; CURRENT APPLICATION NUMBER: US/10/923,115
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05162
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 355
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-923-115-355

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AUAUAUCUAUUUCG 14
      |||:|:|:|:|:|
Db      1 AUAUAUCUAUUUCG 14

RESULT 5
US-10-869-638-467
; Sequence 467, Application US/10869638
; Publication No. US20050119211A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Bharat, Chowhira
; APPLICANT: James, McSwiggen
```

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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Connexin Gene Expression
; FILE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/165 (MEHB04-509)
; CURRENT APPLICATION NUMBER: US/10/869,638
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-869-638-467

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy      1 AUAUACUUAUUUCG 14
Db      1 AUAUACUUAUUUCG 14

RESULT 6
US-10-871-222-703
; Sequence 703, Application US/10871222
; Publication No. US20050119212A1
; GENERAL INFORMATION:
; APPLICANT: Haerberli, Peter
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Mediated Inhibition Fatty Acid Synthase (FAS) and Fatty Acids
; TITLE OF INVENTION: Synthase Ligand (FASL) Gene Expression Using Short Interfering
; TITLE OF INVENTION: Nucleic Acid (siNA)
; FILE REFERENCE: 400/164 (MEHB04-487)
; CURRENT APPLICATION NUMBER: US/10/871,222
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US10/826966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US10/757803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US10/720448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US10/693059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US10/444853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 467
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-869-638-467

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy      1 AUAUACUUAUUUCG 14
Db      1 AUAUACUUAUUUCG 14

RESULT 7
US-10-879-867-437
; Sequence 437, Application US/10879867
; Publication No. US20050124566A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Robin, Howard
; APPLICANT: Gueriolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Myostatin Gene Expression
; FILE REFERENCE: 400/196 (MEHB04-536)
; CURRENT APPLICATION NUMBER: US/10/879,867
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 437
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-879-867-437

Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy      1 AUAUACUUAUUUCG 14
Db      1 AUAUACUUAUUUCG 14
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Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
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Db 1 AUAUAUCUAUUUCG 14

RESULT 8
US-10-883-218-927
; Sequence 927, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/195 (MBHB04-535)
; CURRENT APPLICATION NUMBER: US/10/883,218
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 927
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-883-218-927

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
    |||||
Db 1 AUAUAUCUAUUUCG 14

RESULT 9
US-10-888-226-952
; Sequence 952, Application US/10888226
; Publication No. US20050124569A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Nasseem
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Acetyl-CoA-Carboxylase
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400-199 (MBHB03-710-A)
; CURRENT APPLICATION NUMBER: US/10/888,226
; CURRENT FILING DATE: 2004-07-09
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; PRIOR APPLICATION NUMBER: US 60/486,729
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 955
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 952
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-888-226-952

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
    |||||
Db 1 AUAUAUCUAUUUCG 14

RESULT 10
US-10-892-922-293
; Sequence 293, Application US/10892922
; Publication No. US20050124569A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Guercioli, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of CXCR4 Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400-198
; CURRENT APPLICATION NUMBER: US/10/892,922
; CURRENT FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 293
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-892-922-293

Query Match 100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AUAUAUCUAUUUCG 14
    |||||
Db 1 AUAUAUCUAUUUCG 14

RESULT 11
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US-10-881-118-449  
; Sequence 449, Application US/10881118  
; Publication No. US20050130181A1  
; GENERAL INFORMATION:  
; APPLICANT: McSwiggen, James  
; APPLICANT: Sirna Therapeutics, Inc.  
; TITLE OF INVENTION: RNA Mediated Inhibition of Wingless Gene Expression Using Short  
; TITLE OF INVENTION: Interfering Nucleic Acid (sina)  
; FILE REFERENCE: 400-197 (MHB04-546)  
; CURRENT FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: US/10/881,118  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US10/826966  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US10/757803  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US10/444853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US10/693059  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US60/358580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US60/363124  
; PRIOR FILING DATE: 2002-03-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 449  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-881-118-449

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

RESULT 12  
US-10-861-060-371  
; Sequence 371, Application US/10861060  
; Publication No. US20050137155A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Haerzli, Peter  
; APPLICANT: Chowhira, Bharat  
; TITLE OF INVENTION: RNA Interference Mediated Treatment of Parkinson Disease Using  
; TITLE OF INVENTION: Short Interfering Nucleic Acid (sina)  
; FILE REFERENCE: 400/162 (MHB04-372-A)  
; CURRENT FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US/10/861,060  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: US 10/698,311  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/720,448

QY 1 AUAUAUCUAUUUCG 14  
|||||  
Db 1 AUAUAUCUAUUUCG 14

RESULT 13  
US-10-863-973-1829  
; Sequence 1829, Application US/10863973  
; Publication No. US2005014333A1  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Ivan  
; APPLICANT: Polisky, Barry  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and  
; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering  
; FILE REFERENCE: 400/163 (MHB03-084-D)  
; CURRENT FILING DATE: 2004-06-09  
; PRIOR APPLICATION NUMBER: PCT/US03/04566  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1832  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1829  
; LENGTH: 14  
; TYPE: RNA

; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 10/698311  
; PRIOR FILING DATE: 2003-10-31  
; PRIOR APPLICATION NUMBER: PCT/US04/13456  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 374  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 371  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence  
US-10-861-060-371

Query Match 100.0%; Score 14; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUAUAUCUAUUUCG 14  
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Db 1 AUAUAUCUAUUUCG 14

RESULT 13  
US-10-863-973-1829  
; Sequence 1829, Application US/10863973  
; Publication No. US2005014333A1  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Ivan  
; APPLICANT: Polisky, Barry  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Interleukin and  
; TITLE OF INVENTION: Interleukin Receptor Gene Expression Using Short Interfering  
; FILE REFERENCE: 400/163 (MHB03-084-D)  
; CURRENT FILING DATE: 2004-06-09  
; PRIOR APPLICATION NUMBER: PCT/US03/04566  
; PRIOR FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/US04/16390  
; PRIOR FILING DATE: 2004-05-24  
; PRIOR APPLICATION NUMBER: US 10/826,966  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 10/757,803  
; PRIOR FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 10/720,448  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2003-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1832  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1829  
; LENGTH: 14  
; TYPE: RNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-863-973-1829
Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUAUACUUAUUUCG 14
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Db      1 AUUAUACUUAUUUCG 14

RESULT 14
US-10-922-544-471
; Sequence 471, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/204 (MHB03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 471
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-922-544-471
Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUAUACUUAUUUCG 14
      |||||
Db      1 AUUAUACUUAUUUCG 14

RESULT 15
US-10-923-330-765
; Sequence 765, Application US/10923330
; Publication No. US20050153916A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
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; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
; FILE REFERENCE: 400/209 (MHB02-708-C)
; CURRENT APPLICATION NUMBER: US/10/923,330
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 765
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-923-330-765
Query Match      100.0%; Score 14; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AUUAUACUUAUUUCG 14
      |||||
Db      1 AUUAUACUUAUUUCG 14

Search completed: June 28, 2006, 23:45:30
Job time : 819 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic ; nucleic search, using sw model

Run on: June 28, 2006, 23:31:55 ; Search time 78 Seconds  
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212.243 Million cell updates/sec

Title: US-10-824-036A-3578  
Perfect score: 14  
Sequence: 1 auaaucauauucg 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	11.4	81.4	25	7	US-11-217-529-84996	Sequence 84996, A
4	11.4	81.4	25	7	US-11-217-529-92520	Sequence 92520, A
5	11	78.6	25	7	US-11-217-529-55741	Sequence 55741, A
6	11	78.6	25	7	US-11-217-529-159959	Sequence 159959, A
7	10.8	77.1	25	7	US-11-217-529-49309	Sequence 49309, A
8	10.8	77.1	25	7	US-11-217-529-49452	Sequence 49452, A
9	10.8	77.1	25	7	US-11-217-529-64003	Sequence 64003, A
10	10.8	77.1	25	7	US-11-217-529-64755	Sequence 64755, A
11	10.8	77.1	25	7	US-11-217-529-99687	Sequence 99687, A
12	10.8	77.1	25	7	US-11-217-529-137664	Sequence 137664, A
13	10.8	77.1	25	7	US-11-217-529-166214	Sequence 166214, A
14	10.8	77.1	25	7	US-11-217-529-166369	Sequence 166369, A
15	10.8	77.1	25	7	US-11-217-529-169973	Sequence 169973, A
16	10.4	74.3	19	6	US-10-424-339-1385	Sequence 1385, Ap
C 17	10.4	74.3	19	6	US-10-424-339-1566	Sequence 1566, Ap
18	10.4	74.3	19	7	US-11-254-792-2	Sequence 2, Appli
19	10.4	74.3	19	7	US-11-254-792-4	Sequence 4, Appli
C 20	10.4	74.3	25	7	US-11-217-529-7732	Sequence 7732, Ap
21	10.4	74.3	25	7	US-11-217-529-21009	Sequence 21009, A
22	10.4	74.3	25	7	US-11-217-529-28746	Sequence 28746, A
23	10.4	74.3	25	7	US-11-217-529-37826	Sequence 37826, A
24	10.4	74.3	25	7	US-11-217-529-115068	Sequence 115068, A
25	10.4	74.3	25	7	US-11-217-529-131643	Sequence 131643, A

26	10.4	74.3	25	7	US-11-217-529-152354	Sequence 152354,
27	10.4	74.3	25	7	US-11-217-529-166236	Sequence 166236,
28	10.4	74.3	25	7	US-11-217-529-169553	Sequence 169553,
29	10.4	74.3	25	7	US-11-217-529-169560	Sequence 169560,
30	10.4	74.3	25	7	US-11-217-529-172575	Sequence 172575,
31	10.4	74.3	25	7	US-11-217-529-177198	Sequence 177198,
32	10.4	74.3	25	7	US-11-217-529-177654	Sequence 177654,
33	10.4	74.3	25	7	US-11-217-529-184630	Sequence 184630,
34	10.4	74.3	25	7	US-11-217-529-184635	Sequence 184635,
35	10	71.4	25	7	US-11-217-529-86582	Sequence 86582, A
36	10	71.4	25	7	US-11-217-529-99532	Sequence 99532, A
37	10	71.4	25	7	US-11-217-529-105976	Sequence 105976,
38	10	71.4	25	7	US-11-217-529-112907	Sequence 112907,
39	10	71.4	25	7	US-11-217-529-117458	Sequence 117458,
40	10	71.4	25	7	US-11-217-529-150756	Sequence 150756,
C 41	10	71.4	25	7	US-11-217-529-166399	Sequence 166399,
42	10	71.4	25	7	US-11-217-529-171207	Sequence 171207,
43	10	71.4	25	7	US-11-217-529-189684	Sequence 189684,
44	9.8	70.0	24	6	US-10-415-326-15	Sequence 15, Appl
45	9.8	70.0	24	7	US-11-257-502-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1  
US-11-217-529-101087  
; Sequence 101087, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 101087  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-101087

Query Match 88.6%; Score 12.4; DB 7; Length 25;  
Best Local Similarity 42.9%; Pred. No. 1e+03;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AJAAUUAUUCG 14  
DB 2 ATTATCTATTTCG 15

RESULT 2  
US-11-217-529-114875/c  
; Sequence 114875, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-114875

Query Match      88.6%; Score 12.4; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUUAUCUUAUUCG 14
Db 22 ATATATCTATTTC 9

RESULT 3
US-11-217-529-84996/c
; Sequence 84996, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84996
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-84996

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUUAUCUUAUUC 13
Db 25 ATATATATATTTC 13

RESULT 4
US-11-217-529-92520
; Sequence 92520, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 92520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-92520

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 46.2%; Pred. No. 3.3e+03;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 UAUAUCUUAUUCG 14
Db 3 TATACTATTTCG 15

RESULT 5
US-11-217-529-55741
; Sequence 55741, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55741
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-55741

Query Match      78.6%; Score 11; DB 7; Length 25;
Best Local Similarity 36.4%; Pred. No. 5.4e+03;
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUAUCUUAUU 12
Db 14 TATATCTATTTC 24

RESULT 6
US-11-217-529-159959
; Sequence 159959, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-159959
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us-10-824-036a-3578.sz40.rnpbn

Thu Jun 29 15:49:22 2006

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Query Match      78.6%; Score 11; DB 7; Length 25;
Best Local Similarity 45.5%; Pred. No. 5.4e+03;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      3 AUAUACUUAUUCG 13
|:|:|:|:|:|
Db      2 ATATCTATTTC 12

RESULT 7
US-11-217-529-49309
; Sequence 49309, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49309
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49309

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 6.8e+03;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
|:|:|:|:|:|
Db      10 ATATATCTCTCTCG 23

RESULT 8
US-11-217-529-49452
; Sequence 49452, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49452
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49452

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 35.7%; Pred. No. 6.8e+03;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
|:|:|:|:|:|
Db      3 ATATATCTTTTTC 16

RESULT 9
US-11-217-529-64003
; Sequence 64003, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-64003

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 42.9%; Pred. No. 6.8e+03;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
|:|:|:|:|:|
Db      9 ATATATCTTTTTCG 22

RESULT 10
US-11-217-529-64755
; Sequence 64755, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64755
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-64755

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 35.7%; Pred. No. 6.8e+03;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUAUACUUAUUCG 14
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Db      3 ATATATCTTTTTCG 16
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RESULT 11  
US-11-217-529-99687  
; Sequence 99687, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 99687  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-99687

Query Match 77.1%; Score 10.8; DB 7; Length 25;  
Best Local Similarity 42.9%; Pred. No. 6.8e+03;  
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AUAUACUUAUUCG 14  
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Db 3 ATATATCCATTTCG 16

RESULT 12  
US-11-217-529-137664  
; Sequence 137664, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 137664  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-137664

Query Match 77.1%; Score 10.8; DB 7; Length 25;  
Best Local Similarity 42.9%; Pred. No. 6.8e+03;  
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AUAUACUUAUUCG 14  
|:|:|:|:|:|:|  
Db 6 AGATATTTATTTTCG 19

RESULT 13  
US-11-217-529-166214  
; Sequence 166214, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 166214  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-166214

Query Match 77.1%; Score 10.8; DB 7; Length 25;  
Best Local Similarity 42.9%; Pred. No. 6.8e+03;  
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AUAUACUUAUUCG 14  
|:|:|:|:|:|:|  
Db 1 ATTATCTACTTCG 14

RESULT 14  
US-11-217-529-166369  
; Sequence 166369, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 166369  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-166369

Query Match 77.1%; Score 10.8; DB 7; Length 25;  
Best Local Similarity 35.7%; Pred. No. 6.8e+03;  
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AUAUACUUAUUCG 14  
|:|:|:|:|:|:|  
Db 2 ATATTTCTATTTAG 15

RESULT 15  
US-11-217-529-169973  
; Sequence 169973, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO

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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 169973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-169973

Query Match      77.1%; Score 10.8; DB 7; Length 25;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      1 AUUAUUCUUAUUCG 14
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Db       2 ATATTACTACTTCG 15

Search completed: June 28, 2006, 23:46:54
Job time : 79 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2006, 22:58:28 ; Search time 4276 Seconds  
(without alignments)  
183.085 Million cell updates/sec

Title: US-10-824-036A-3578  
Perfect score: 14  
Sequence: 1 aaaucauauucy 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 115878

Minimum DB seq length: 0

Maximum DB-seq length: 40

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_hic.\*  
7: gb\_est2.\*  
8: gb\_est7.\*  
9: gb\_est8.\*  
10: gb\_est9.\*  
11: gb\_gss1.\*  
12: gb\_gss2.\*  
13: gb\_gss3.\*  
14: gb\_gss4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	12	85.7	36	11	B2291752	B2291752 SALK_1217
3	12	85.7	36	11	B2291754	B2291754 SALK_1217
4	11.4	81.4	20	11	A2958303	A2958303 2M0225106
5	11.4	81.4	25	11	A1074222	A1074222 oz85a01.x
6	11.4	81.4	30	14	BX946341	BX946341 Arabidops
7	11.4	81.4	31	14	CT011025	CT011025 KBrH118M0
8	11.4	81.4	32	14	ATH520505	AJ520505 Arabidops
9	11.4	81.4	33	14	BX946340	BX946340 Arabidops
10	11.4	81.4	34	14	DR61F19S	AL982633 Danio rer
11	11	78.6	32	11	A1587460	A1587460 tr51a02.x
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13	11	78.6	38	12	CC793445	CC793445 SALK_0143
14	10.8	77.1	24	11	BH853216	BH853216 SALK_0761
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16	10.8	77.1	38	11	BH810085	BH810085 SALK_0406
17	10.8	77.1	39	11	AU264278	AU264278 AU264278
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22	10.4	74.3	23	14	TA300F12P	AL490817 T. brucei
23	10.4	74.3	25	1	AI761999	AI761999 wh50909.x
24	10.4	74.3	25	11	AZ371135	AZ371135 1M0122N04
25	10.4	74.3	25	11	AZ625569	AZ625569 1M0465112
26	10.4	74.3	25	14	ATH528692	AJ528692 Arabidops
27	10.4	74.3	25	14	ATH528882	AJ528882 Arabidops
28	10.4	74.3	27	5	CD576920	CD576920 2L_B03_21
29	10.4	74.3	27	11	BZ353129	BZ353129 SALK_1198
30	10.4	74.3	27	14	TA175807Q	AL475337 T. brucei
31	10.4	74.3	28	11	AZ786457	AZ786457 2M0032B03
32	10.4	74.3	29	11	AZ796712	AZ796712 2M0052M03
33	10.4	74.3	29	13	CZ486260	CZ486260 f03682-5p
34	10.4	74.3	30	11	AZ366827	AZ366827 1M0116B17
35	10.4	74.3	30	13	CZ484387	CZ484387 f01890-3p
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37	10.4	74.3	31	14	BX532321	BX532321 Arabidops
38	10.4	74.3	31	14	BX532876	BX532876 Arabidops
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40	10.4	74.3	32	11	AZ345920	AZ345920 1M0080I23
41	10.4	74.3	32	13	CZ293526	CZ293526 P075802 G
42	10.4	74.3	32	13	CL658452	CL658452 PRI0131C-
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ALIGNMENTS

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LOCUS  
DEFINITION  
ywc3h05.sl Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA  
clone IMAGE:256953 3' similar to gb.L03558 CYSTATIN B  
(HUMAN); contains Alu repetitive element;; mRNA sequence.

ACCESSION  
N30120  
VERSION  
EST.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens

REFERENCE  
AUTHORS  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,K., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE  
The WashU-Merck EST Project

JOURNAL  
Unpublished (1995)

COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

TEL: 314 286 1800

FAX: 314 286 1810

EMAIL: est@watson.wustl.edu

High quality sequence stops: 4

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: ml3 -40 forward

High quality sequence stop: 4.

Location/Qualifiers

1..34

/organism="Homo sapiens"

/mol\_type="mRNA"

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/db\_xref="taxon:9606"

/clone="IMAGE:256953"

/dev\_stage="two placentae: one from 8 weeks and another

from 9 weeks post conception"  
/lab\_host="DRI0B (ampicillin resistant)"  
/clone\_lib="Soares placentas\_8to9weeks\_2NbHP8to9w"  
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer (5'  
TGTTACCAATCTGAAGTGGGAGCGCGGATTTTTTTTTTTT 3')  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library constructed by Bento Soares and  
M.Fatima Bonaldo."

ORIGIN

Query Match 86.6%; Score 12.4; DB 10; Length 34;  
Best Local Similarity 42.9%; Pred. No. 8.7e+04;  
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUUAUCUAUUUC 14  
Db 12 ATATATCTATTTC 25

RESULT 2  
LOCUS BZ291752/c 36 bp DNA linear GSS 24-OCT-2002  
DEFINITION SALK\_121715.40.90-x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_121715.40.90.x, genomic  
survey sequence.

ACCESSION BZ291752  
VERSION BZ291752.1 GI:24337754  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmermann,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within 300 bases of the 3' end of  
At2g18700 and 300 bases of the 3' end of At2g18710.  
Class: TDNA tagged.

FEATURES

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Location/Qualifiers  
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/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;

Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 2 UAUAUCUAUUUC 13  
Db 24 TATATCTATTTC 13

RESULT 3  
LOCUS BZ291754/c 36 bp DNA linear GSS 24-OCT-2002  
DEFINITION SALK\_121717.36.85-x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_121717.36.85.x, genomic  
survey sequence.

ACCESSION BZ291754  
VERSION BZ291754.1 GI:24337762  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmermann,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within 300 bases of the 3' end of  
At2g18700 and 300 bases of the 3' end of At2g18710.  
Class: TDNA tagged.

FEATURES

source  
1..36  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_121717.36.85.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 85.7%; Score 12; DB 11; Length 36;  
Best Local Similarity 41.7%; Pred. No. 1.4e+05;  
Matches 5; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 UAUAUCUAUUUC 13  
Db 24 TATATCTATTTC 13

RESULT 4  
LOCUS AZ958303/c 20 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0225106R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0225106 R, genomic survey sequence.

ACCESSION AZ958303  
VERSION AZ958303.1 GI:13829530  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM	Mus musculus	EST.	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.	KEYWORDS	Homo sapiens
AUTHORS	1 (bases 1 to 20) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	REFERENCE	1 (bases 1 to 25) NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL	Unpublished (2000)	AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0225 row: 1 column: 06 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 20. Location/Qualifiers 1. .20 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /db_xref="taxon:10090" /clone_lib="UUC2M0225106" /sex="Female" /lab_host="E. coli strain XL10-Gold, T1-resistant, P-" /clone_lib="Mouse 10kb plasmid UUC2M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	COMMENT	This clone is available royalty-free through LNL; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Trace considered overall poor quality Insert Length: 418 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1. .25 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1682088" /tissue_type="senescent fibroblast" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares senescent fibroblasts NBHSF" /note="Vector: pT7T3D (Pharmacia) with a modified polylinker V-TYPE; phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTCGAGCGCGCCGATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
FEATURES	source	LOCUS	30 bp DNA linear GSS 05-APR-2004
ORIGIN		DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-761A05-024641, genomic survey sequence.
	Query Match 81.4%; Score 11.4; DB 1; Length 25; Best Local Similarity 46.2%; Pred. No. 2.8e+05; Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;	ACCESSION	EX946341 GI:42596027
	Qy 1 AUAUAUCUAUUC 13  : : : : :	VERSION	EX946341.1
	Db 20 ATATATCTATTAC 8	KEYWORDS	GSS.
		SOURCE	Arabidopsis thaliana (thale cress)
		ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
		REFERENCE	1 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana Bioinformatics 19 (11), 1441-1442 (2003) 12874060
		AUTHORS	2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
		JOURNAL	
		PUBMED	
		REFERENCE	
		AUTHORS	
		TITLE	
		LOCUS	25 bp mRNA linear EST 01-OCT-1998
		DEFINITION	oz85a01.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1682088 3' similar to TR:Q25802 Q25802 FRAMESHIFT. ; mRNA sequence.
		ACCESSION	AI074222
		VERSION	AI074222.1 GI:3400866
		ORIGIN	
	Query Match 81.4%; Score 11.4; DB 11; Length 20; Best Local Similarity 46.2%; Pred. No. 2.8e+05; Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;		
	Qy 1 AUAUAUCUAUUC 13  : : : : :		
	Db 19 ATATATCTATTAC 7		
		RESULT 5	
		LOCUS	AI074222/c
		DEFINITION	oz85a01.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1682088 3' similar to TR:Q25802 Q25802 FRAMESHIFT. ; mRNA sequence.
		ACCESSION	AI074222
		VERSION	AI074222.1 GI:3400866

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse Genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**

Direct Submission  
 Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F24B18. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
 Location/Qualifiers  
 1. .30

**FEATURES**  
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/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-761A05-024641"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**ORIGIN**

Query Match 81.4%; Score 11.4; DB 14; Length 30;  
 Best Local Similarity 38.5%; Pred. No. 2.8e+05;  
 Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 AUAUACUUAUUC 13  
 |:|:|:|:|:|  
**Db** 21 ATATATATATTC 9

**RESULT 7**  
**CT011025**  
**LOCUS**  
**DEFINITION**  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**

CT011025  
 KBrH118M09 genomic clone, KBrH (HindIII) BAC library Brassica rapa subsp. pekinensis, genomic survey sequence.  
 CT011025  
 GSS.  
 CT011025.1 GI:71479066  
 Brassica rapa subsp. pekinensis  
 Brassica rapa subsp. pekinensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Brassica.

**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**

Vahoevoer, P., Holtgraewe, D. and Weishaar, B.  
 BAC end sequences of Brassica rapa  
 Unpublished  
 2 (bases 1 to 31)  
 Li, Y. and Weishaar, B.  
 Direct Submission  
 Submitted (09-AUG-2005) Weishaar B., Bielefeld University, Institute for Genome Research, Universitaetsstrasse 25, D-33594 Bielefeld, Germany

**COMMENT**

Contact: Bernd Weishaar  
 Bielefeld University, Institute for Genome Research  
 Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:  
 bernd.weishaar@uni-bielefeld.de  
 BAC end sequences of Brassica rapa BAC clone KBrH118M09; generated as contribution to the 'Multinational Brassica rapa Sequencing Project'. Seq primer: sp6B ATTTAGGTGACACTATAG  
 Class: BAC ends.  
 Location/Qualifiers  
 1. .31  
 /organism="Brassica rapa subsp. pekinensis"  
/mol\_type="genomic DNA"  
/strain="Chifu type 401-42"  
/cultivar="Chifu"  
/sub\_species="pekinensis"  
/db\_xref="taxon:51351"  
/clone="KBrH118M09"  
/clone\_lib="KBrH, Brassica rapa HindIII BAC library GF-SCF-1002. Vector: pCUGIBac1"  
/lab\_host="E.coli DH10B"

**FEATURES**  
 source

Query Match 81.4%; Score 11.4; DB 14; Length 31;  
 Best Local Similarity 38.5%; Pred. No. 2.8e+05;  
 Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 AUAUACUUAUUC 13  
 |:|:|:|:|:|  
**Db** 17 ATTTATCTATTC 29

**RESULT 8**  
**ATH520505**  
**LOCUS**  
**DEFINITION**  
**ACCESSION**  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**

ATH520505  
 Arabidopsis thaliana T-DNA flanking sequence, left border, clone 036C02, genomic survey sequence.  
 AJ520505.1 GI:26788741  
 GSS; left border; T-DNA flanking sequence.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.

**REFERENCE**  
**AUTHORS**

Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 EMBO Rep. 3 (12), 1152-1157 (2002)  
 12446565

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

2 (bases 1 to 32)  
 Balzergue, S.  
 Direct Submission  
 Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publicines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).  
 Location/Qualifiers  
 1. .32

**FEATURES**  
 source

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewska"



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/db xref="taxon:3702"
/clone="036C02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1. 32
misc_feature
/notes="T-DNA flanking sequence
left border"

ORIGIN
Query Match 81.4%; Score 11.4; DB 14; Length 32;
Best Local Similarity 38.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
|:|:|:|:|:|
Db 13 ATATATCTTTTC 25

RESULT 9
BX946340/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-761A05-024593,
genomic survey sequence.
ACCESSION
BX946340
VERSION
BX946340.1 GI:42596026
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 Li.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
GABI-Kat Simplesearch: a flanking sequence tag (fST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
REFERENCE
2 Rosso,M.G., Li.Y., Strizhov,N., Reis,B., Dekker,K. and
Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
REFERENCE
3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
REFERENCE
4 Li.Y., Strizhov,N., Rosso,M.G. and Weishaar,B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
F24818. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .33
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"

ORIGIN
Query Match 81.4%; Score 11.4; DB 14; Length 32;
Best Local Similarity 38.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
|:|:|:|:|:|
Db 13 ATATATCTTTTC 25

RESULT 10
DR61F19S/c
LOCUS
DEFINITION
Danio rerio genomic clone DKEY-61F19, genomic survey sequence.
ACCESSION
AL982633
VERSION
AL982633.1 GI:25187375
KEYWORDS
GSS.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 61F19. 61F19 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .34
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61F19"
/tissue_type="Testis"
/notes="Vector pIndigoBAC-536"

ORIGIN
Query Match 81.4%; Score 11.4; DB 14; Length 34;
Best Local Similarity 46.2%; Pred. No. 2.8e+05;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
|:|:|:|:|:|
Db 29 ATATATCTATATC 17

RESULT 11
AI587460
LOCUS
DEFINITION
t551402.x1 NCI CCAP Paul Homo sapiens cDNA clone IMAGE:2221802 3',
similar to gb|U10284 CALNEXIN PRECURSOR (HUMAN), mRNA sequence.
ACCESSION
AI587460
VERSION
AI587460.1 GI:4573901
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 32)

```

```

/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ37514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 81.4%; Score 11.4; DB 14; Length 33;
Best Local Similarity 38.5%; Pred. No. 2.8e+05;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
|:|:|:|:|:|
Db 24 ATATATATATTC 12

RESULT 10
DR61F19S/c
LOCUS
DEFINITION
Danio rerio genomic clone DKEY-61F19, genomic survey sequence.
ACCESSION
AL982633
VERSION
AL982633.1 GI:25187375
KEYWORDS
GSS.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 61F19. 61F19 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .34
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-61F19"
/tissue_type="Testis"
/notes="Vector pIndigoBAC-536"

ORIGIN
Query Match 81.4%; Score 11.4; DB 14; Length 34;
Best Local Similarity 46.2%; Pred. No. 2.8e+05;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 AUAUACUUAUUC 13
|:|:|:|:|:|
Db 29 ATATATCTATATC 17

RESULT 11
AI587460
LOCUS
DEFINITION
t551402.x1 NCI CCAP Paul Homo sapiens cDNA clone IMAGE:2221802 3',
similar to gb|U10284 CALNEXIN PRECURSOR (HUMAN), mRNA sequence.
ACCESSION
AI587460
VERSION
AI587460.1 GI:4573901
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 32)

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Matches      5;  Conservative      6;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  AUAUAUCUUAU 11
|:|:|:|:|:|
Db      27  ATATATCTATT 37

RESULT 14
BH853216
LOCUS      24 bp      DNA      linear      GSS 13-JUN-2002
DEFINITION SALK_076188.27.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_076188.27.55.x, genomic
            survey sequence.
ACCESSION  BH853216
VERSION    BH853216.1  GI:21424087
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1  (bases 1 to 24)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jekker,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL    Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At5gl0720.
            Class: TDNA tagged.
FEATURES   Location/Qualifiers
            source          1..24
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /strain="Col-0"
                        /db_xref="taxon:3702"
                        /clone="SALK_076188.27.55.x"
                        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                        /notes="PCR was performed on Arabidopsis thaliana lines
                        each of which contains one or more TDNA insertion
                        elements. The resultant fragment for each line was
                        directly sequenced to determine the genomic sequence at
                        the site of insertion. Details of the protocols used can
                        be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      77.1%; Score 10.8; DB 11; Length 24;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches      7;  Conservative      5;  Mismatches      2;  Indels      0;  Gaps      0;

QY      1  AUAUAUCUUAUUCG 14
|:|:|:|:|:|
Db      1  ATATATCTACTCG 14

RESULT 15
AZ789033
LOCUS      25 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 2M0036H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0036H02 R, genomic survey sequence.
ACCESSION  AZ789033
VERSION    AZ789033.1  GI:12929432
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1  (bases 1 to 25)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert length: 10000 Std Error: 0.00
            Plate: 0036 row: H column: 02
            Seq primer: CACACAGGAACACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES       Location/Qualifiers
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                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC2M0036H02"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /notes="Vector: PWD42nv; Purified genomic DNA from M.
                        musculus C57BL/6J (male) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adaptor DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of PWD42 (GI4732114|GB|AF129072.1), a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adaptor mouse DNA was annealed to
                        adaptor vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."

ORIGIN
Query Match      77.1%; Score 10.8; DB 11; Length 25;
Best Local Similarity 35.7%; Pred. No. 5.6e+05;
Matches      5;  Conservative      7;  Mismatches      2;  Indels      0;  Gaps      0;

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